

SEQUENCE LISTING

<110> Munger, Karl and Syken, Josh

<120> Methods and Reagents to Regulate Apoptosis

<130> HMV-054.01

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<170> PatentIn version 3.0

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Gly Arg Gly Ala Arg Pro Pro Arg Glu Gly Val Val Gly Ala Trp Leu
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Ser Arg Lys Leu Ser Val Pro Ala Phe Ala Ser Ser Leu Thr Ser Cys
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Gly Pro Arg Ala Leu Leu Thr Leu Arg Pro Gly Val Ser Leu Thr Gly
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Pro Leu Ala Lys Glu Asp Tyr Tyr Gln Ile Leu Gly Val Pro Arg Asn
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Ala Ser Gln Lys Glu Ile Lys Lys Ala Tyr Tyr Gln Leu Ala Lys Lys
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tat cac cct gac aca aat aag gat gat ccc aaa gcc aag gag aag ttc 436
Tyr His Pro Asp Thr Asn Lys Asp Asp Pro Lys Ala Lys Glu Lys Phe
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 35 40 45

Ala Ser Ser Leu Thr Ser Cys Gly Pro Arg Ala Leu Leu Thr Leu Arg
 50 55 60

Pro Gly Val Ser Leu Thr Gly Thr Lys His Asn Pro Phe Ile Cys Thr
 65 70 75 80

Ala Ser Phe His Thr Ser Ala Pro Leu Ala Lys Glu Asp Tyr Tyr Gln
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Ile Leu Gly Val Pro Arg Asn Ala Ser Gln Lys Glu Ile Lys Lys Ala
 100 105 110

Tyr Tyr Gln Leu Ala Lys Lys Tyr His Pro Asp Thr Asn Lys Asp Asp
 115 120 125

Pro Lys Ala Lys Glu Lys Phe Ser Gln Leu Ala Glu Ala Tyr Glu Val
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19900802.001

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 180 185 190

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 195 200 205

Gln Glu Tyr Phe Met Glu Leu Thr Phe Asn Gln Ala Ala Lys Gly Val
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Asn Lys Glu Phe Thr Val Asn Ile Met Asp Thr Cys Glu Arg Cys Asn
 225 230 235 240

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 245 250 255

Gly Gly Ser Gly Met Glu Thr Ile Asn Thr Gly Pro Phe Val Met Arg
 260 265 270

Ser Thr Cys Arg Arg Cys Gly Gly Arg Gly Ser Ile Ile Ile Ser Pro
 275 280 285

Cys Val Val Cys Arg Gly Ala Gly Gln Ala Lys Gln Lys Lys Arg Val
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 325 330 335

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 370 375 380

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Tyr Gly Asp His Tyr Ile His Ile Lys Ile Arg Val Pro Lys Arg Leu
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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: mRNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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GGC GTG GTG GGG GCA TGG CTG AGC CGC AAG CTG AGC GTC CCC GCC TTT	144
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CCT GGT GTC AGC CTT ACA GGA ACA AAA CAT AAC CCT TTC ATT TGT ACT	240
Pro Gly Val Ser Leu Thr Gly Thr Lys His Pro Phe Ile Cys Thr	
65 70 75 80	
GCC TCC TTC CAC ACG AGT GCC CCT TTG GCC AAA GAA GAT TAT TAT CAG	288
Ala Ser Phe His Thr Ser Ala Pro Leu Ala Lys Glu Asp Tyr Tyr Gln	
85 90 95	
ATA TTA GGA GTG CCT CGA AAT GCC AGC CAG AAA GAG ATC AAG AAA GCC	336
Ile Leu Gly Val Pro Arg Asn Ala Ser Gln Lys Glu Ile Lys Lys Ala	
100 105 110	
TAT TAT CAG CTT GCC AAG AAG TAT CAC CCT GAC ACA AAT AAG GAT GAT	384

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CCC	AAA	GCC	AAG	GAG	AAG	TTC	TCC	CAG	CTG	GCA	GAA	GCC	TAT	GAG	GTT	432	
Pro	Lys	Ala	Lys	Glu	Lys	Phe	Ser	Gln	Leu	Ala	Glu	Ala	Tyr	Glu	Val		
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Leu	Ser	Asp	Glu	Val	Lys	Arg	Lys	Gln	Tyr	Asp	Ala	Tyr	Gly	Ser	Ala		
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Gly	Phe	Asp	Pro	Gly	Ala	Ser	Gly	Ser	Gln	His	Ser	Tyr	Trp	Lys	Gly		
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GGC	CCC	ACT	GTG	GAC	CCC	GAG	GAG	CTG	TTC	AGG	AAG	ATC	TTT	GGC	GAG	576	
Gly	Pro	Thr	Val	Asp	Pro	Glu	Glu	Leu	Phe	Arg	Lys	Ile	Phe	Gly	Glu		
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Phe	Ser	Ser	Ser	Ser	Phe	Gly	Asp	Phe	Gln	Thr	Val	Phe	Asp	Gln	Pro		
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CAG	GAA	TAC	TTC	ATG	GAG	TTG	ACA	TTC	AAT	CAA	GCT	GCA	AAG	GGG	GTC	672	
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Asn	Lys	Glu	Phe	Thr	Val	Asn	Ile	Met	Asp	Thr	Cys	Glu	Arg	Cys	Asn		
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GGC	AAG	GGG	AAC	GAG	CCC	GGC	ACC	AAG	GTG	CAG	CAT	TGC	CAC	TAC	TGT	768	
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GGC	GGC	TCC	GGC	ATG	GAA	ACC	ATC	AAC	ACA	GGC	CCT	TTT	GTG	ATG	CGT	816	
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Cys	Val	Val	Cys	Arg	Gly	Ala	Gly	Gln	Ala	Lys	Gln	Lys	Lys	Arg	Val		
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Met	Ile	Pro	Val	Pro	Ala	Gly	Val	Glu	Asp	Gly	Gln	Thr	Val	Arg	Met		
					310					315					320		
CCT	GTG	GGA	AAA	AGG	GAA	ATT	TTC	ATT	ACG	TTC	AGG	GTG	CAG	AAA	AGC	1008	
Pro	Val	Gly	Lys	Arg	Glu	Ile	Phe	Ile	Thr	Phe	Arg	Val	Gln	Lys	Ser		
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CCT	GTG	TTC	CGG	AGG	GAC	GGC	GCA	GAC	ATC	CAC	TCC	GAC	CTC	TTT	ATT	1056	
Pro	Val	Phe	Arg	Arg	Asp	Gly	Ala	Asp	Ile	His	Ser	Asp	Leu	Phe	Ile		
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Tyr	Glu	Thr	Ile	Asn	Val	Thr	Ile	Pro	Pro	Gly	Thr	Gln	Thr	Asp	Gln		
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Tyr	Gly	Asp	His	Tyr	Ile	His	Ile	Lys	Ile	Arg	Val	Pro	Lys	Arg	Leu		
				405				410						415			
ACG	AGC	CGG	CAG	CAG	AGC	CTG	ATC	CTG	AGC	TAC	GCC	GAG	GAC	GAG	ACA	1296	

Thr	Ser	Arg	Gln	Gln	Ser	Leu	Ile	Leu	Ser	Tyr	Ala	Glu	Asp	Glu	Thr		
			420					425					430				
GAT	GTG	GAG	GGG	ACG	GTG	AAC	GGC	GTC	ACC	CTC	ACC	AGC	TCT	GGT	GGC	1344	
Asp	Val	Glu	Gly	Thr	Val	Asn	Gly	Val	Thr	Leu	Thr	Ser	Ser	Gly	Gly		
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AGC	ACC	ATG	GAT	AGC	TCC	GCA	GGA	AGC	AAG	GCT	AGG	CGT	GAG	GCT	GGG	1392	
Ser	Thr	Met	Asp	Ser	Ser	Ala	Gly	Ser	Lys	Ala	Arg	Arg	Glu	Ala	Gly		
	450					455				460							
GAG	GAC	GAG	GAG	GGA	TTC	CTT	TCC	AAA	CTT	AAG	AAA	ATG	TTT	ACC	TCA	1440	
Glu	Asp	Glu	Glu	Gly	Phe	Leu	Ser	Lys	Leu	Lys	Lys	Met	Phe	Thr	Ser		
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TGA																	

1443

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 480 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

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			20					25					30				
Gly	Val	Val	Gly	Ala	Trp	Leu	Ser	Arg	Lys	Leu	Ser	Val	Pro	Ala	Phe		
		35				40					45						
Ala	Ser	Ser	Leu	Thr	Ser	Cys	Gly	Pro	Arg	Ala	Leu	Leu	Thr	Leu	Arg		
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Pro	Gly	Val	Ser	Leu	Thr	Gly	Thr	Lys	His	Asn	Pro	Phe	Ile	Cys	Thr		
65				70					75					80			
Ala	Ser	Phe	His	Thr	Ser	Ala	Pro	Leu	Ala	Lys	Glu	Asp	Tyr	Tyr	Gln		
			85					90					95				
Ile	Leu	Gly	Val	Pro	Arg	Asn	Ala	Ser	Gln	Lys	Glu	Ile	Lys	Lys	Ala		
	100						105					110					
Tyr	Tyr	Gln	Leu	Ala	Lys	Lys	Tyr	His	Pro	Asp	Thr	Asn	Lys	Asp	Asp		
	115					120					125						
Pro	Lys	Ala	Lys	Glu	Lys	Phe	Ser	Gln	Leu	Ala	Glu	Ala	Tyr	Glu	Val		
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Leu	Ser	Asp	Glu	Val	Lys	Arg	Lys	Gln	Tyr	Asp	Ala	Tyr	Gly	Ser	Ala		
145				150					155					160			
Gly	Phe	Asp	Pro	Gly	Ala	Ser	Gly	Ser	Gln	His	Ser	Tyr	Trp	Lys	Gly		
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Phe	Ser	Ser	Ser	Ser	Phe	Gly	Asp	Phe	Gln	Thr	Val	Phe	Asp	Gln	Pro		
	195					200					205						
Gln	Glu	Tyr	Phe	Met	Glu	Leu	Thr	Phe	Asn	Gln	Ala	Ala	Lys	Gly	Val		
	210					215					220						
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Ser	Thr	Cys	Arg	Arg	Cys	Gly	Gly	Arg	Gly	Ser	Ile	Ile	Ile	Ser	Pro		
	275					280					285						
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Pro Val Gly Lys Arg Glu Ile Phe Ile Thr Phe Arg Val Gln Lys Ser		
	325	330
Pro Val Phe Arg Arg Asp Gly Ala Asp Ile His Ser Asp Leu Phe Ile		
	340	345
Ser Ile Ala Gln Ala Leu Leu Gly Gly Thr Ala Arg Ala Gln Gly Leu		
	355	360
Tyr Glu Thr Ile Asn Val Thr Ile Pro Pro Gly Thr Gln Thr Asp Gln		
	370	375
Lys Ile Arg Met Gly Gly Lys Gly Ile Pro Arg Ile Asn Ser Tyr Gly		
385	390	395
Tyr Gly Asp His Tyr Ile His Ile Lys Ile Arg Val Pro Lys Arg Leu		
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Thr Ser Arg Gln Gln Ser Leu Ile Leu Ser Tyr Ala Glu Asp Glu Thr		
	420	425
Asp Val Glu Gly Thr Val Asn Gly Val Thr Leu Thr Ser Ser Gly Gly		
	435	440
Ser Thr Met Asp Ser Ser Ala Gly Ser Lys Ala Arg Arg Glu Ala Gly		
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Glu Asp Glu Glu Gly Phe Leu Ser Lys Leu Lys Lys Met Phe Thr Ser		
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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: mRNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1359

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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CCG CGG CTG CCG GCT ATA TCG GGT AGA GGG GCC CGG CCG CCC AGG GAG	96
Pro Arg Leu Pro Ala Ile Ser Gly Arg Gly Ala Arg Pro Pro Arg Glu	
20 25 30	
GGC GTG GTG GGG GCA TGG CTG AGC CGC AAG CTG AGC GTC CCC GCC TTT	144
Gly Val Val Gly Ala Trp Leu Ser Arg Lys Leu Ser Val Pro Ala Phe	
35 40 45	
GCG TCT TCC CTG ACC TCT TGC GGC CCC CGA GCG CTG CTG ACA TTG AGA	192
Ala Ser Ser Leu Thr Ser Cys Gly Pro Arg Ala Leu Leu Thr Leu Arg	
50 55 60	
CCT GGT GTC AGC CTT ACA GGA ACA AAA CAT AAC CCT TTC ATT TGT ACT	240
Pro Gly Val Ser Leu Thr Gly Thr Lys His Asn Pro Phe Ile Cys Thr	
65 70 75 80	
GCC TCC TTC CAC ACG AGT GCC CCT TTG GCC AAA GAA GAT TAT TAT CAG	288
Ala Ser Phe His Thr Ser Ala Pro Leu Ala Lys Glu Asp Tyr Tyr Gln	
85 90 95	
ATA TTA GGA GTG CCT CGA AAT GCC AGC CAG AAA GAG ATC AAG AAA GCC	336
Ile Leu Gly Val Pro Arg Asn Ala Ser Gln Lys Glu Ile Lys Lys Ala	
100 105 110	
TAT TAT CAG CTT GCC AAG AAG TAT CAC CCT GAC ACA AAT AAG GAT GAT	384

Tyr	Tyr	Gln	Leu	Ala	Lys	Lys	Tyr	His	Pro	Asp	Thr	Asn	Lys	Asp	Asp	
		115					120					125				
CCC	AAA	GCC	AAG	GAG	AAG	TTC	TCC	CAG	CTG	GCA	GAA	GCC	TAT	GAG	GTT	432
Pro	Lys	Ala	Lys	Glu	Lys	Phe	Ser	Gln	Leu	Ala	Glu	Ala	Tyr	Glu	Val	
		130					135					140				
TTG	AGT	GAT	GAG	GTG	AAG	AGG	AAG	CAG	TAC	GAT	GCC	TAC	GGC	TCT	GCA	480
Leu	Ser	Asp	Glu	Val	Lys	Arg	Lys	Gln	Tyr	Asp	Ala	Tyr	Gly	Ser	Ala	
		145				150					155				160	
GGC	TTC	GAT	CCT	GGG	GCC	AGC	GGC	TCC	CAG	CAT	AGC	TAC	TGG	AAG	GGA	528
Gly	Phe	Asp	Pro	Gly	Ala	Ser	Gly	Ser	Gln	His	Ser	Tyr	Trp	Lys	Gly	
				165					170					175		
GGC	CCC	ACT	GTG	GAC	CCC	GAG	GAG	CTG	TTC	AGG	AAG	ATC	TTT	GGC	GAG	576
Gly	Pro	Thr	Val	Asp	Pro	Glu	Glu	Leu	Phe	Arg	Lys	Ile	Phe	Gly	Glu	
			180					185					190			
TTC	TCA	TCC	TCT	TCA	TTT	GGA	GAT	TTC	CAG	ACC	GTG	TTT	GAT	CAG	CCT	624
Phe	Ser	Ser	Ser	Ser	Phe	Gly	Asp	Phe	Gln	Thr	Val	Phe	Asp	Gln	Pro	
		195					200					205				
CAG	GAA	TAC	TTC	ATG	GAG	TTG	ACA	TTC	AAT	CAA	GCT	GCA	AAG	GGG	GTC	672
Gln	Glu	Tyr	Phe	Met	Glu	Leu	Thr	Phe	Asn	Gln	Ala	Ala	Lys	Gly	Val	
		210				215					220					
AAC	AAG	GAG	TTC	ACC	GTG	AAC	ATC	ATG	GAC	ACG	TGT	GAG	CGC	TGC	AAC	720
Asn	Lys	Glu	Phe	Thr	Val	Asn	Ile	Met	Asp	Thr	Cys	Glu	Arg	Cys	Asn	
		225			230				235						240	
GGC	AAG	GGG	AAC	GAG	CCC	GGC	ACC	AAG	GTG	CAG	CAT	TGC	CAC	TAC	TGT	768
Gly	Lys	Gly	Asn	Glu	Pro	Gly	Thr	Lys	Val	Gln	His	Cys	His	Tyr	Cys	
			245					250						255		
GGC	GGC	TCC	GGC	ATG	GAA	ACC	ATC	AAC	ACA	GGC	CCT	TTT	GTG	ATG	CGT	816
Gly	Gly	Ser	Gly	Met	Glu	Thr	Ile	Asn	Thr	Gly	Pro	Phe	Val	Met	Arg	
			260				265					270				
TCC	ACG	TGT	AGG	AGA	TGT	GGT	GGC	CGC	GGC	TCC	ATC	ATC	ATA	TCG	CCC	864
Ser	Thr	Cys	Arg	Arg	Cys	Gly	Gly	Arg	Gly	Ser	Ile	Ile	Ile	Ser	Pro	
		275				280						285				
TGT	GTG	GTC	TGC	AGG	GGA	GCA	GGA	CAA	GCC	AAG	CAG	AAA	AAG	CGA	GTG	912
Cys	Val	Val	Cys	Arg	Gly	Ala	Gly	Gln	Ala	Lys	Gln	Lys	Lys	Arg	Val	
		290				295					300					
ATG	ATC	CCT	GTG	CCT	GCA	GGA	GTC	GAG	GAT	GGC	CAG	ACC	GTG	AGG	ATG	960
Met	Ile	Pro	Val	Pro	Ala	Gly	Val	Glu	Asp	Gly	Gln	Thr	Val	Arg	Met	
		305			310				315						320	
CCT	GTG	GGA	AAA	AGG	GAA	ATT	TTC	ATT	ACG	TTC	AGG	GTG	CAG	AAA	AGC	1008
Pro	Val	Gly	Lys	Arg	Glu	Ile	Phe	Ile	Thr	Phe	Arg	Val	Gln	Lys	Ser	
			325					330					335			
CCT	GTG	TTC	CGG	AGG	GAC	GGC	GCA	GAC	ATC	CAC	TCC	GAC	CTC	TTT	ATT	1056
Pro	Val	Phe	Arg	Arg	Asp	Gly	Ala	Asp	Ile	His	Ser	Asp	Leu	Phe	Ile	
			340				345					350				
TCT	ATA	GCT	CAG	GCT	CTT	CTT	GGG	GGA	ACA	GCC	AGA	GCC	CAG	GGC	CTG	1104
Ser	Ile	Ala	Gln	Ala	Leu	Leu	Gly	Gly	Thr	Ala	Arg	Ala	Gln	Gly	Leu	
		355				360						365				
TAC	GAG	ACG	ATC	AAC	GTG	ACG	ATC	CCC	CCT	GGG	ACT	CAG	ACA	GAC	CAG	1152
Tyr	Glu	Thr	Ile	Asn	Val	Thr	Ile	Pro	Pro	Gly	Thr	Gln	Thr	Asp	Gln	
		370				375					380					
AAG	ATT	CGG	ATG	GGT	GGG	AAA	GGC	ATC	CCC	CGG	ATT	AAC	AGC	TAC	GGC	1200
Lys	Ile	Arg	Met	Gly	Gly	Lys	Gly	Ile	Pro	Arg	Ile	Asn	Ser	Tyr	Gly	
		385			390					395					400	
TAC	GGA	GAC	CAC	TAC	ATC	CAC	ATC	AAG	ATA	CGA	GTT	CCA	AAG	AGG	CTA	1248
Tyr	Gly	Asp	His	Tyr	Ile	His	Ile	Lys	Ile	Arg	Val	Pro	Lys	Arg	Leu	
			405					410					415			
ACG	AGC	CGG	CAG	CAG	AGC	CTG	ATC	CTG	AGC	TAC	GCC	GAG	GAC	GAG	ACA	1296

Thr	Ser	Arg	Gln	Gln	Ser	Leu	Ile	Leu	Ser	Tyr	Ala	Glu	Asp	Glu	Thr		
			420					425					430				
GAT	GTG	GAG	GGG	ACG	GTG	AAC	GGC	GTC	ACC	CTC	ACC	AGC	TCT	GGA	AAA		1344
Asp	Val	Glu	Gly	Thr	Val	Asn	Gly	Val	Thr	Leu	Thr	Ser	Ser	Gly	Lys		
		435					440					445					
AGA	TCC	ACT	GGA	AAC	TAG												1362
Arg	Ser	Thr	Gly	Asn													
			450														

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Ala	Ala	Arg	Cys	Ser	Thr	Arg	Trp	Leu	Val	Val	Val	Gly	Thr			
1				5				10					15				
Pro	Arg	Leu	Pro	Ala	Ile	Ser	Gly	Arg	Gly	Ala	Arg	Pro	Pro	Arg	Glu		
			20				25					30					
Gly	Val	Val	Gly	Ala	Trp	Leu	Ser	Arg	Lys	Leu	Ser	Val	Pro	Ala	Phe		
			35				40					45					
Ala	Ser	Ser	Leu	Thr	Ser	Cys	Gly	Pro	Arg	Ala	Leu	Leu	Thr	Leu	Arg		
			50			55					60						
Pro	Gly	Val	Ser	Leu	Thr	Gly	Thr	Lys	His	Asn	Pro	Phe	Ile	Cys	Thr		
					70					75				80			
Ala	Ser	Phe	His	Thr	Ser	Ala	Pro	Leu	Ala	Lys	Glu	Asp	Tyr	Tyr	Gln		
				85					90					95			
Ile	Leu	Gly	Val	Pro	Arg	Asn	Ala	Ser	Gln	Lys	Glu	Ile	Lys	Lys	Ala		
			100				105						110				
Tyr	Tyr	Gln	Leu	Ala	Lys	Lys	Tyr	His	Pro	Asp	Thr	Asn	Lys	Asp	Asp		
			115				120					125					
Pro	Lys	Ala	Lys	Glu	Lys	Phe	Ser	Gln	Leu	Ala	Glu	Ala	Tyr	Glu	Val		
			130			135					140						
Leu	Ser	Asp	Glu	Val	Lys	Arg	Lys	Gln	Tyr	Asp	Ala	Tyr	Gly	Ser	Ala		
			145			150				155				160			
Gly	Phe	Asp	Pro	Gly	Ala	Ser	Gly	Ser	Gln	His	Ser	Tyr	Trp	Lys	Gly		
				165					170					175			
Gly	Pro	Thr	Val	Asp	Pro	Glu	Glu	Leu	Phe	Arg	Lys	Ile	Phe	Gly	Glu		
			180					185					190				
Phe	Ser	Ser	Ser	Ser	Phe	Gly	Asp	Phe	Gln	Thr	Val	Phe	Asp	Gln	Pro		
			195				200					205					
Gln	Glu	Tyr	Phe	Met	Glu	Leu	Thr	Phe	Asn	Gln	Ala	Ala	Lys	Gly	Val		
			210				215				220						
Asn	Lys	Glu	Phe	Thr	Val	Asn	Ile	Met	Asp	Thr	Cys	Glu	Arg	Cys	Asn		
					230					235				240			
Gly	Lys	Gly	Asn	Glu	Pro	Gly	Thr	Lys	Val	Gln	His	Cys	His	Tyr	Cys		
				245					250					255			
Gly	Gly	Ser	Gly	Met	Glu	Thr	Ile	Asn	Thr	Gly	Pro	Phe	Val	Met	Arg		
			260					265					270				
Ser	Thr	Cys	Arg	Arg	Cys	Gly	Gly	Arg	Gly	Ser	Ile	Ile	Ile	Ser	Pro		
			275				280					285					
Cys	Val	Val	Cys	Arg	Gly	Ala	Gly	Gln	Ala	Lys	Gln	Lys	Lys	Arg	Val		
			290			295					300						
Met	Ile	Pro	Val	Pro	Ala	Gly	Val	Glu	Asp	Gly	Gln	Thr	Val	Arg	Met		
			305			310				315				320			
Pro	Val	Gly	Lys	Arg	Glu	Ile	Phe	Ile	Thr	Phe	Arg	Val	Gln	Lys	Ser		

				325					330					335			
Pro	Val	Phe	Arg	Arg	Asp	Gly	Ala	Asp	Ile	His	Ser	Asp	Leu	Phe	Ile		
			340					345					350				
Ser	Ile	Ala	Gln	Ala	Leu	Leu	Gly	Gly	Thr	Ala	Arg	Ala	Gln	Gly	Leu		
		355					360					365					
Tyr	Glu	Thr	Ile	Asn	Val	Thr	Ile	Pro	Pro	Gly	Thr	Gln	Thr	Asp	Gln		
	370					375					380						
Lys	Ile	Arg	Met	Gly	Gly	Lys	Gly	Ile	Pro	Arg	Ile	Asn	Ser	Tyr	Gly		
385				390				395						400			
Tyr	Gly	Asp	His	Tyr	Ile	His	Ile	Lys	Ile	Arg	Val	Pro	Lys	Arg	Leu		
			405					410					415				
Thr	Ser	Arg	Gln	Gln	Ser	Leu	Ile	Leu	Ser	Tyr	Ala	Glu	Asp	Glu	Thr		
		420					425					430					
Asp	Val	Glu	Gly	Thr	Val	Asn	Gly	Val	Thr	Leu	Thr	Ser	Ser	Gly	Lys		
	435					440					445						
Arg	Ser	Thr	Gly	Asn													
	450																

FOOTNOTES